

S. Huff.

1642
#7

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/426,814

DATE: 12/11/2000
TIME: 22:47:55

INPUT SET: S36192.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

ENTERED

(i) APPLICANT: Holmes, Stephen D.
Gross, Mitchell S.
Sylvester, Daniel R.

(ii) TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
Treatment of IL4 Mediated Disorders

(iii) NUMBER OF SEQUENCES: 58

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SmithKline Beecham Corporation
(B) STREET: Corporate Intellectual Property, UW2220 - 709
Swedeland Rd.
(C) CITY: King of Prussia
(D) STATE: PA
(E) COUNTRY: USA
(F) ZIP: 19406-2799

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/426,814
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/612,929
(B) FILING DATE:
(A) APPLICATION NUMBER: US 08/136,783
(B) FILING DATE: 14-OCT-1993

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Sutton, Jeffrey A.
(B) REGISTRATION NUMBER: 34,028
(C) REFERENCE/DOCKET NUMBER: P50186-2

(ix) TELECOMMUNICATION INFORMATION:

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DEC 15 2000

TECH CENTER 1600/2900

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47 (A) TELEPHONE: (215) 270-5024
48 (B) TELEFAX: (215) 270-5090
49
50
51

52 (2) INFORMATION FOR SEQ ID NO:1:
53

54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 396 base pairs
56 (B) TYPE: nucleic acid
57 (C) STRANDEDNESS: double
58 (D) TOPOLOGY: unknown
59

60 (ii) MOLECULE TYPE: cDNA
61

62 (ix) FEATURE:
63 (A) NAME/KEY: CDS
64 (B) LOCATION: 1..396
65
66
67
68
69
70

71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
72

73	ATG GAG ACA GAC ACA ATC CTG CTA TGG GTG CTG CTG CTC TGG GTT CCA	48
74	Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro	
75	1 5 10 15	
76		
77	GGC TCC ACT GGT GAC ATT GTG CTG ACC CAA TCT CCA GCT TCT TTG GCT	96
78	Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala	
79	20 25 30	
80		
81	GTG TCT CTA GGG CAG AGG GCC ACC ATC TCC TGC AAG GCC AGC CAA AGT	144
82	Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser	
83	35 40 45	
84		
85	GTT GAT TAT GAT GGT GAT AGT TAT ATG AAC TGG TAC CAA CAG AAA CCA	192
86	Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro	
87	50 55 60	
88		
89	GGA CAG CCA CCC AAA CTC CTC ATC TAT GCT GCA TCC AAT CTA GAA TCT	240
90	Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser	
91	65 70 75 80	
92		
93	GGG ATC CCA GCC AGG TTT AGT GGC AGT GGG TCT GGG ACA GAC TTC ACC	288
94	Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr	
95	85 90 95	
96		
97	CTC AAC ATC CAT CCT GTG GAG GAG GAG GAT GCT GCA ACC TAT TAC TGT	336
98	Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys	
99	100 105 110	

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100
101 CAG CAA AGT AAT GAG GAT CCT CCG ACG TTC GGT GGA GGC ACC AAG CTG 384
102 Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
103 115 120 125
104
105 GAA ATC AAA CGG 396
106 Glu Ile Lys Arg
107 130
108
109

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

120
121 Met Glu Thr Asp Thr Ile Leu Leu Trp Val Leu Leu Leu Trp Val Pro
122 1 5 10 15
123
124 Gly Ser Thr Gly Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala
125 20 25 30
126
127 Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys Lys Ala Ser Gln Ser
128 35 40 45
129
130 Val Asp Tyr Asp Gly Asp Ser Tyr Met Asn Trp Tyr Gln Gln Lys Pro
131 50 55 60
132
133
134 Gly Gln Pro Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Ser
135 65 70 75 80
136
137 Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
138 85 90 95
139
140 Leu Asn Ile His Pro Val Glu Glu Glu Asp Ala Ala Thr Tyr Tyr Cys
141 100 105 110
142
143 Gln Gln Ser Asn Glu Asp Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu
144 115 120 125
145
146 Glu Ile Lys Arg
147 130
148
149

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

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153          (A) LENGTH: 483 base pairs
154          (B) TYPE: nucleic acid
155          (C) STRANDEDNESS: double
156          (D) TOPOLOGY: unknown
157
158      (ii) MOLECULE TYPE: cDNA
159
160      (ix) FEATURE:
161          (A) NAME/KEY: CDS
162          (B) LOCATION: 64..483
163
164      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
165
166      GAATTCGCGG CCGCTATGCA GGGACAATCA GCAGCAGCAA TGAGGAAGTA AGCCTGTGCA      60
167
168      GAT ATG AAC AGG CTT ACT TCC TCA TTG CTG CTG CTG ATT GTC CCT GCA      108
169      Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Leu Ile Val Pro Ala
170      1 5 10 15
171
172      TAT GTC CTG TCC CAG GTT ACT CTG AAA GAG TCT GGC CCT GGG ATA TTG      156
173      Tyr Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu
174      20 25 30
175
176      CAG CCC TCC CAG ACC CTC AGT CTG ACT TGT TCT TTC TCT GGG TTT TCA      204
177      Gln Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser
178      35 40 45
179
180      CTG AGC ACT TCT GGT ATG GGT GTG AGC TGG ATT CGT CAG CCT TCA GGA      252
181      Leu Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly
182      50 55 60
183
184      AAG GGT CTG GAG TGG CTG GCA CAC ATT TAC TGG GAT GAT GAC AAG CGC      300
185      Lys Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg
186      65 70 75
187
188      TAT AAC CCA TCC CTG AAG AGC CGG CTC ACA ATC TCC AAG GAT ACC TCC      348
189      Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
190      80 85 90 95
191
192      AGC AAC CAG GTA TTC CTC AAG ATC ACC AGT GTG GAC ACT GCA GAT ACT      396
193      Ser Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr
194      100 105 110
195
196
197      GCC ACA TAC TAC TGT GCT CGA AGA GAG ACT GTG TTC TAC TGG TAC TTC      444
198      Ala Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe
199      115 120 125
200
201      GAT GTC TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC TCA      483
202      Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser
203      130 135 140
204
205

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206 (2) INFORMATION FOR SEQ ID NO:4:

207

208 (i) SEQUENCE CHARACTERISTICS:

209 (A) LENGTH: 140 amino acids

210 (B) TYPE: amino acid

211 (D) TOPOLOGY: linear

212

213 (ii) MOLECULE TYPE: protein

214

215 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

216

217 Met Asn Arg Leu Thr Ser Ser Leu Leu Leu Ile Val Pro Ala Tyr

218 1 5 10 15

219

220 Val Leu Ser Gln Val Thr Leu Lys Glu Ser Gly Pro Gly Ile Leu Gln

221 20 25 30

222

223 Pro Ser Gln Thr Leu Ser Leu Thr Cys Ser Phe Ser Gly Phe Ser Leu

224 35 40 45

225

226 Ser Thr Ser Gly Met Gly Val Ser Trp Ile Arg Gln Pro Ser Gly Lys

227 50 55 60

228

229 Gly Leu Glu Trp Leu Ala His Ile Tyr Trp Asp Asp Asp Lys Arg Tyr

230 65 70 75 80

231

232 Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Ser

233 85 90 95

234

235 Asn Gln Val Phe Leu Lys Ile Thr Ser Val Asp Thr Ala Asp Thr Ala

236 100 105 110

237

238 Thr Tyr Tyr Cys Ala Arg Arg Glu Thr Val Phe Tyr Trp Tyr Phe Asp

239 115 120 125

240

241 Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser

242 130 135 140

243

244

245 (2) INFORMATION FOR SEQ ID NO:5:

246

247 (i) SEQUENCE CHARACTERISTICS:

248 (A) LENGTH: 60 base pairs

249 (B) TYPE: nucleic acid

250 (C) STRANDEDNESS: double

251 (D) TOPOLOGY: unknown

252

253 (ii) MOLECULE TYPE: cDNA

254

255 (ix) FEATURE:

256 (A) NAME/KEY: CDS

257 (B) LOCATION: 1..60

258

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/426,814

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SEQUENCE MISSING ITEM REPORT
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SEQUENCE CORRECTION REPORT
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Line	Original Text	Corrected Text
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